

FIGURE 3. BLAST results of Coiled-Coil regions of GAS 40 with other Streptococcus bacteria

3(a) BLAST alignment of amino acid sequence of GAS 40 including the first coiled-coil region with SpA precursor of *Streptococcus gordonii*

>gi|25990270|gb|AAC44101.3| streptococcal surface protein A precursor
[*Streptococcus gordonii*]
Length = 1575
>ref|NP_268623.1| putative surface exclusion protein [*Streptococcus pyogenes*]
Length = 873

Score = 63.2 bits (152), Expect = 5e-11
Identities = 65/293 (22%), Positives = 124/293 (42%), Gaps = 13/293 (4%)

Query: 112 QDQTSKGTATTAENAQKQAEIKSDYAKQA---EEIKKTTEAYKKEVEAHQAETDKIN
167

Q + D+ + T A N + K + ++A + ++KT K E+ K
Sbjct: 33 QVADDRASGETKASNTHDSSLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTT
92

Query: 168 AENKAAEDKYQEDLKAHQAEVEKINTANATAKAEYEAKLAQYQKDLAAVQKANEDSQLDY
227

AE +++ + KA + E A+++ A+ A++Q++L A + ++Q D
Sbjct: 93 AEINHLKEQQDNEQKALTSAQEIYTNLASSSEETLLAQGAHQRELATETELHNAQADQ
152

Query: 228 QNKLSAYQAELARVQKANAEAKEAYE--KAVKENTAKNAALQAENEAIKQRNETAKANYD
285

+K +A + A + A++ E K ++N AK A+ + +AI + +TA N
Sbjct: 153 HSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAITKAAQTANDNTK
212

Query: 286 AAMKQYEADLAAIKKAKEDNDADYQAKLAAAYQAELARVQKANADAKAAYEKAVEENTAKN
345

A + E A ++ K +LAA +A LA + + K++ + N
Sbjct: 213 ALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEKEAELSRLKSSAPSTQDSIVGNN
272

Query: 346 TAIQAEN---EAIKQRNAA---AKATYEAALKQYEADLAAAKKANEDSDADYQ 392

T + E +K+ A+ A+Y K++ AD AK + + YQ
Sbjct: 273 TMKAPQGYPLEELKKLEASGYIGSASYNYYKEH-ADQIIAKASPGNQLNQYQ 324

FIGURE 3, CONT. BLAST results of Coiled-Coil regions of GAS 40 with other Streptococcus bacteria

3(b) BLAST alignment of amino acid sequence of GAS 40 including the first coiled-coil region with SpB precursor of *Streptococcus gordonii*

>gi|25055226|gb|AAC44102.3| streptococcal surface protein B precursor [Streptococcus gordonii]

Length = 1499

>ref|NP_268623.1| putative surface exclusion protein [Streptococcus pyogenes]

Length = 873

Score = 54.3 bits (129), Expect = 2e-08
Identities = 53/226 (23%), Positives = 98/226 (43%), Gaps = 13/226 (5%)

Query: 111 QDQTSDKGTATTAENAQKQAEIKSDYAKQA---EEIKKTTEAYKKEVEAHQAETDKIN
166

Q + D+ + T A N + K + ++A + ++KT K E+ K
Sbjct: 33 QVKADDRASGETKASNTHDDSLPKPETIQEAKATIDAVEKTLSSQKAELTELATALTKTT
92

Query: 167 AENKAAEDKYQEDLKAHQAEVEKINTANATAKAEYEAKLAQYQKDLAAVQKANEDSQLDY
226

AE +++ + KA + E A+++ A+ A++Q++L A + ++Q D
Sbjct: 93 AEINHLKEQQDNEQKALTSAQEIYTNLASSSEETLLAQGAEHQRELTATETELHNAQADQ
152

Query: 227 QNKLSAYQAELARV--QXXXXXXXXXXXXXXXXXNTAKNAALQAENEAIKQRNETAKANYD
284

+K +A + A + + N AK A+ + +AI + +TA N
Sbjct: 153 HSKETALSEQKASISAETTRAQDLVEQVKTSEQNIAKLNAMISNPDAITKAAQTANDNTK
212

Query: 285 AAMKQYE---ADL---AAIKKAKEDNDADYQAKLAAYQAELARVQ 323

A + E ADL A +KK + A +A LA +AEL+R++
Sbjct: 213 ALSSELEKAKADLENQKAKVKKQLTEELAAQKAALAEKEAELSRLLK 258

FIGURE 3, CONT. BLAST results of Coiled-Coil regions of GAS 40 with other Streptococcus bacteria

3(c) BLAST alignment of amino acid sequence of GAS 40 including the first coiled-coil region with Surface Protein PspA precursor of *Streptococcus pneumoniae*

```
>gi|282335|pir|A41971 surface protein pspA precursor - Streptococcus pneumoniae  
>ref|NP_268623.1| putative surface exclusion protein [Streptococcus pyogenes]
```

Length = 873

Score = 48.1 bits (113), Expect = 6e-07
Identities = 46/200 (23%), Positives = 89/200 (44%), Gaps = 23/200 (11%)

```
Query: 139 KTKFNTVRAMVVPEPEQLAETK-----KKSEEAKQKAPELTKKLEEAKAKLEE-AEKK  
190
```

```
          +TK +          +P+PE + E K          K + K + EL L + A++ E++  
Sbjct: 43 ETKASNTHTDSDLPKPETIQEAKATIDAVEKTLSSQKAELELATALTKTTAEINHLKEQQ  
102
```

```
Query: 191 ATEAKQKVDABEVAPQAKIAELENQVHRLEQELKEIDSESESDYAKEGFRAPLQSKLDAK  
250
```

```
          E K A+E+          + E + + + +E+ +E+E + + + ++ L +  
Sbjct: 103 DNEQKALTSAQEIYTNLASSSEETLLAQGAHQRELTATETELHNAQADQHSKETALSEQ  
162
```

```
Query: 251 KAKLS----KLEELSDKIDELDAEIAKLEDQL-----KAAEENNNVEDYFKEGLEKTI  
299
```

```
          KA +S          + ++L +++          + IAKL          +          KAA+ N+          LEK  
Sbjct: 163 KASISAETTRAQDLVEQVKTSEQNIAKLNAMI SNPDAITKAAQTANDNTKALSSELEKA-  
221
```

```
Query: 300 AAKKAELEKTEADLKKAVNE 319
```

```
          KA+LE +A +KK + E  
Sbjct: 222 ---KADLENQKAKVKKQLTE 238
```

FIGURE 3, CONT. BLAST results of Coiled-Coil regions of GAS 40 with other Streptococcus bacteria

3(d) BLAST alignment of amino acid sequence of GAS 40 including the second coiled-coil region with SpB precursor of *Streptococcus gordonii*

>gi|23380384|gb|AAN18299.1| immunoreactive protein Se89.9 (fragment)
[Streptococcus equi]

Length = 210

>ref|NP_268623.1| putative surface exclusion protein [Streptococcus pyogenes]

Length = 873

Score = 173 bits (438), Expect = 4e-45
Identities = 98/209 (46%), Positives = 144/209 (68%)

Query: 1 ESDIVDATRFSTTEIPKSGQVIDRSASIQALTNDIASIKGKIASLESRLADPSSEAEVTA
60

ES+I + RF+ T I G D + + +++ IA+IKGK++SLE+RL+ EA++ A

Sbjct: 509 ESNIANHQRFNKTPIKAVGSTKDYAQRVGTVSDTIAAIKGVSSLENRLSAIHQEADIMA
568

Query: 61 AQAKISQLQHLEAAQAKSHKLDQQVEQLANTKDSLRTQLLAAKEEQAQLKANLDKALAL
120

AQAK+SQLQ +L + +S L+ QV QL +TK SLRT+LLAAK +QAQL+A D++LA

Sbjct: 569 AQAKVSQLQGKLASTLKQSDSLNLQVRQLNDTKGSLRTELLAAKAKQAQLEATRDQSLAK
628

Query: 121 LASSKATLHKLEAAMEEAKARVAGLASQKAQLEDLLAFEKNPNRIELAQEKVAAAKKALA
180

LAS KA LH+ EA E+A ARV L ++KA L+ L F+ NPNR+++ +E++ K+ LA

Sbjct: 629 LASLKAALHQTEALAEQAAARVTALVAKKAHLQYLRDFKLNPNRLQVIRERIDNTKQDLA
688

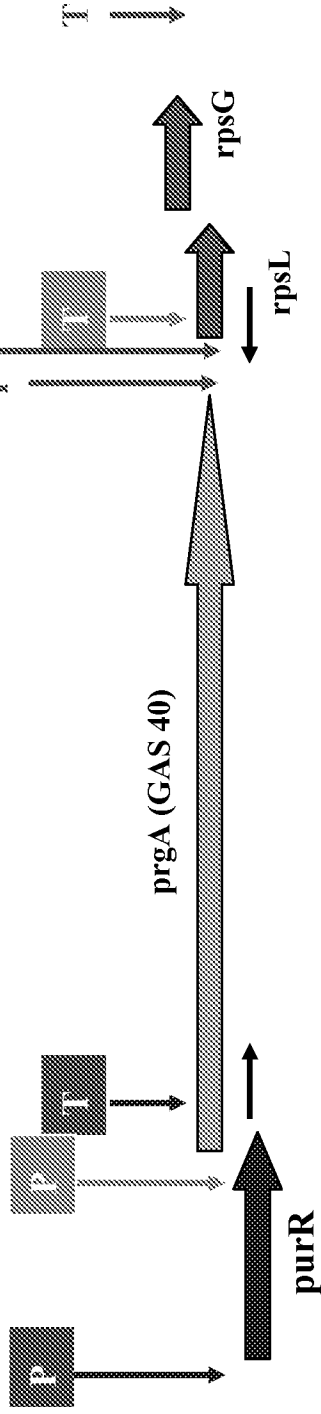
Query: 181 DTEDKLLAAQASLSDLQAQRARLQLSIAT 209

T LL AQ +L+ LQA+++ L+ +IAT

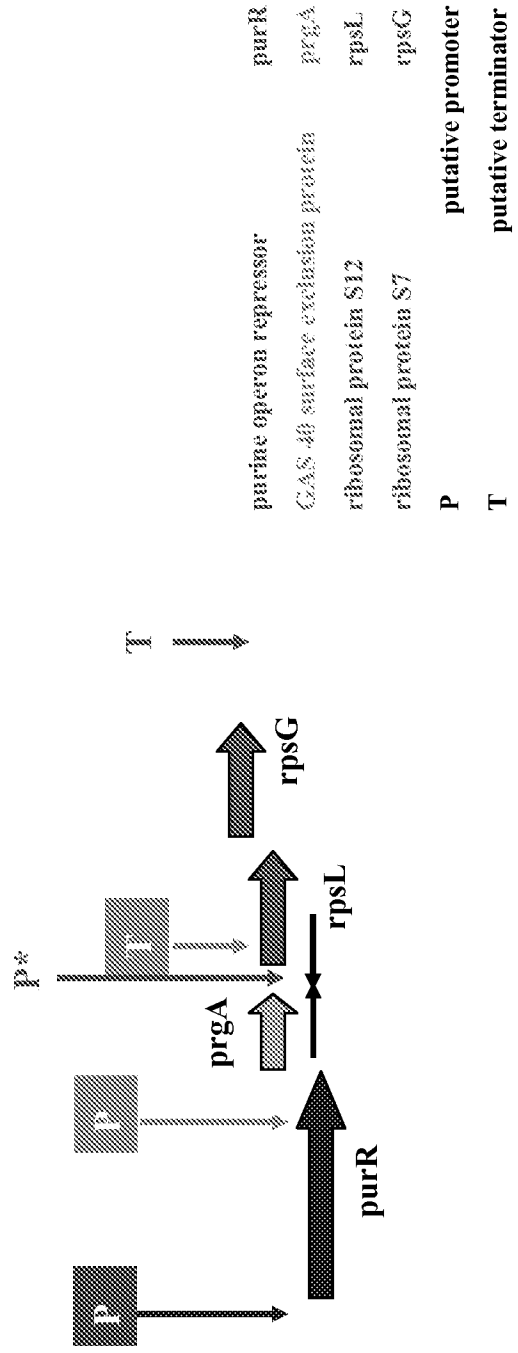
Sbjct: 689 KTTSSLLNAQEALAAALQAKQSSLEATIAT 717

Figure 5

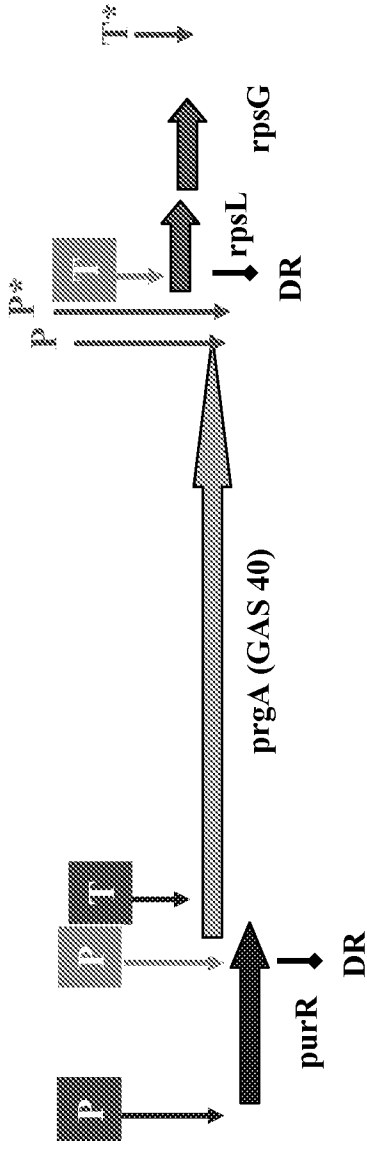
5A
 location of
 gas40
 within GAS
 genome



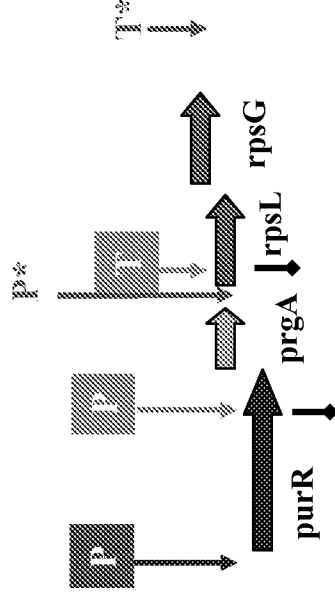
5B
 Δ gas40
 deletion
 mutant



5C
 direct repeats
 surrounding GAS 40
 within wild type genome



5D
 location of direct
 repeats within Δ gas40



5E
 corresponding
 genomic region
 within GBS

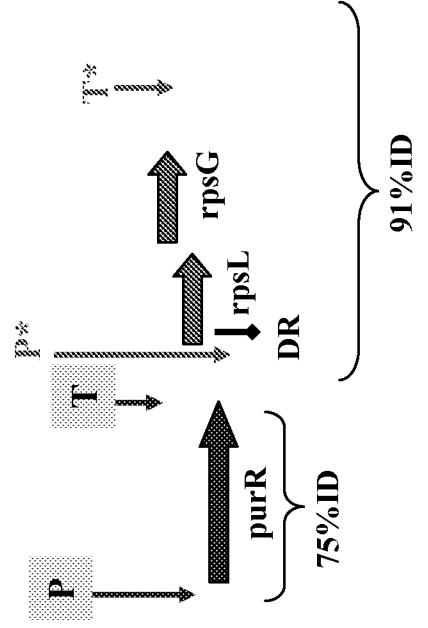


Figure 5, cont.